

Table 1

Colony Grouping	Comment
5hw, 7hw, 8hw, 25hw	Hybridize with <i>groES/groEL</i> probe
10hw, 15hw, 17hw, 22hw	Hybridize with <i>map2</i> probe
16hw, 26hw	Cross-hybridizing insert DNA
18hw, 20hw, 24hw	Cross-hybridizing insert DNA

Table 2

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
1hw	4,360	<i>Rickettsia prowazekii</i> dimethyladenosine transferase	PIR:C71673	1 to 372	No	14,090	41/51	94 2e-19
1hw		<i>Synechocystis</i> sp. triosephosphate isomerase	PIR:S76293	611 to 1,333	Yes	26,456	37/47	153 5e-37
1hw		<i>Brucella abortus</i> cell surface protein precursor	PIR:IMBKBB	1,333 to 2,313	Yes	35,907	31/42	171 3e-42
1hw		<i>Rickettsia prowazekii</i> o-sialoglycoprotein endopeptidase	PIR:E71711	2,611 to 3,366	Yes	27,832	46/59	217 3e-56
1hw		None		4,065 to 4,286	Yes	8,941		
3hw	4,055	<i>Rickettsia prowazekii</i> valine-tRNA ligase	SP:Q9ZCN6	1 to 1321	No	51,512	52/65	494 1e-138
3hw		None		1 to 605	No	22,109		
3hw		<i>Thiobacillus ferrooxidans</i> glutamate-cysteine ligase	PIR:E59237	3,507 to 4,055	No	20,930	38/51	100 2e-20

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
4hw	4,913	<i>Rickettsia prowazekii</i> hypothetical ferripyochelin binding protein	PIR:F71655	196 to 714	Yes	18,651	45/55	162 5e-40
4hw		<i>Rickettsia prowazekii</i> dihydroipoamide acetyltransferase component	GP:CAA14646	1,298 to 2,506	Yes	44,415	53/65	397 1e-110
4hw		None		3,686 to 4,913	No	45,965		
6hw	6,190	<i>Rickettsia prowazekii</i> ribonucleoside reductase, beta chain	PIR:B71655	1,835 to 2,809	Yes	38,331	73/79	416 1e-116
6hw		None		3,126 to 5,072	Yes	72,921		
9hw	2,778	<i>Thermotoga maritima</i> AraM protein	PIR:C72396	1 to 551	No	20,547	31/45	84 1e-15
9hw		<i>Rickettsia prowazekii</i> ATP synthase A chain	PIR:G71709	1,487 to 2,218	Yes	27,030	51/64	230 4e-60
9hw		<i>Rickettsia prowazekii</i> ATP synthase C chain	GP:CAA14493	2,288 to 2,509	Yes	7,774	53/62	82 4e-16

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
9hw		<i>Malawimonas jakobiformis</i> mitochondrion ATP synthase F0 subunit 8	GP:AAG13695	2,519 to 2,778	No	10,146	30/48	50 6e-06
11hw	4,122	<i>Rickettsia prowazekii</i> iron-sulfur cofactor synthesis protein	PIR:B71652	459 to 2,027	Yes	57,773	42/50	256 6e-67
11hw		<i>Rickettsia prowazekii</i> iron-sulfur cofactor synthesis protein	PIR:A71652	2,099 to 3,340	Yes	46,211	64/72	535 1e-151
11hw		<i>Drosophila melanogaster</i> NIFU-like protein	SP:Q9ZD61	3,375 to 3,788	Yes	14,727	72/79	198 2e-50
12hw	3,814	<i>Halobacterium sp.</i> gas vesicle protein gene	GP:AAC82836	144 to 953	Yes	28,644	29/39	872e-16
12hw		<i>Caulobacter crescentus</i> polar organelle development protein	GP:AAC72820	1177 to 3,814	No	93,955	35/44	231 1e-59
12hw		None		1,594 to 3,291	Yes	59,939		
12hw		None		2,789 to 3,334	Yes	20,061		

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
13hw	3,900	<i>Rickettsia prowazekii</i> cytosol aminopeptidase	SP:P27888	816 to 2,318	Yes	54,438	46/55	397 1e-110
13hw		Zebrafish phosphoribosylamine-glycine ligase	GP:AAF71749	2,486 to 3,124	Yes	23,247	46/57	180 1e-44
13hw		<i>Rickettsia prowazekii</i> lipote-protein ligase B	GP:CAA15299	3,548 to 3,900	No	13,682	38/55	97 8e-20
14hw	4,369	None		1 to 1,147	No	42,556		
14hw		<i>Helicobacter pylori</i> membrane protein (lpp*)	PIR:B64703	1,354 to 4,119	Yes	103,319	31/42**	39 0.06
18hw	3,500	<i>Coxiella burnetii</i> outer membrane protein	GP:BAA20508	511 to 1,263	Yes	28,127	27/37	94 8e-19
18hw		None		1,275 to 3,500	No	83,566		
19hw	4,750	<i>Rickettsia prowazekii</i> probable integrase/recombinase	PIR:B71643	1 to 371	No	14,622	31/47	76 1e-13

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
19hw		<i>Trypanosoma brucei</i> glycosomal glycerol 3-phosphate dehydrogenase	GP:CAA62581	632 to 1,615	Yes	35,696	35/48	186 2e-46
19hw		<i>Rickettsia prowazekii</i> nitrogen assimilation regulatory protein	GP:CAA15010	2467 to 3882	Yes	53,490	49/60	399 1e-110
19hw		<i>Rickettsia prowazekii</i> cell division protein ftsQ	PIR:F71679	4,154 to 4,750	No	22,540	26/38	71 4e-12
21hw	4,544	<i>Methanococcus jannaschii</i> phosphoribosylformyl- glycinamide synthase	PIR:G64457	1 to 1,566	No	57,998	31/43	178 3e-44
21hw		<i>Pneumocystis carinii</i> folic acid synthesis protein	PIR:S28666	2,252 to 2,776	Yes	20,044	34/45	95 9e-20
21hw		None		3,985 to 4,544	No	20,776		
23hw	4,483	<i>Escherichia coli</i> hypothetical transmembrane protein	PIR:H64942	624 to 1,331	Yes	26,641	31/47	106 6e-23

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
23hw		<i>Synechocystis</i> sp. ribosome-binding factor A	PIR:S76285	2,526 to 2,873	Yes	13,311	27/39	51 1e-06
23hw		<i>Rickettsia prowazekii</i> translation initiation factor IF-2	GP:CAA15001	2,870 to 4,483	No	58,862	49/63	496 1e-139
26hw	3,829	<i>Rickettsia prowazekii</i> tryptophanyl-tRNA ligase	PIR:A71706	1 to 780	No	29,340	49/60	240 3e-63
26hw		<i>Macaca mulatta</i> cell surface mucin (tandem repeat)	GP:AAF82403	2,361 to 3,416	Yes	35,652	35/39	105 8e-22
26hw		None (except to 26hw orf above)		3,530 to 3,829	No	10,882		
27hw	4,460	None (omp*)		369 to 1,094	Yes	27,631		
27hw		<i>Rickettsia prowazekii</i> DNA-3-methyladenine glycosidase	PIR:A71692	2,149 to 2,715	Yes	21,241	51/60	152 1e-36
27hw		None (lpp*)		3,382 to 3,900	Yes	19,396		
27hw		None		3,369 to 3,608	Yes	8,634		

Table 2--continued

Clone	Insert size	Homologous sequence	Accession number	Clone sequence (nt)	Entire gene	M.wt.	Identity/ Similarity	High Probability Score (E value)
23hw		<i>Synechocystis</i> sp. ribosome-binding factor A	PIR:S76285	2,526 to 2,873	Yes	13,311	27/39	51 1e-06
2gd	2,008	<i>Rickettsia prowazekii</i> unknown peptide	PIR:B71697	1 to 348	No	13,139	23/34	41 0.001
3gd	3,829	<i>Pyrococcus horikoshi</i> hypothetical NADH dehydrogenase (ubiquinone)	GP:BAA30538	605 to 2,083	Yes	54,158	33/48	218 1e-55
3gd		None		2,311 to 2,610	Yes	11,460		
3gd		<i>Pseudomonas putida</i> toluene tolerance protein, ABC transporter (omp*)	GP:AAD17959	3,209 to 3,658	Yes	16,181	36/50	89 2e-17
4gd	226	<i>Neisseria meningitidis</i> tldD protein	GP:AAF42385	1 to 226	No	7,816	73/83	115 4e-26
5gd	160	None	5/6 reading frames open					
6gd	299	<i>Rickettsia prowazekii</i> unknown peptide	PIR:D71672	1 to 299	No	11,079	33/45	44 2e-04
7gd	2,104 381	<i>Ureaplasma urealyticum</i> DNA ligase 1e-104	GP:AAF30527	180 to 2104	No	74,059	38/51	

Table 3		
Immunizing lysate	# surviving/total	% survival
Experiment 1		
1-5hw	4/10	40
6-10hw	3/7	43
11-15hw	2/8	25
16-20hw	6/10	60
21-25hw	8/9	89
vector	0/9	0
none	1/10	10
Experiment 2		
26-27hw+1-3gd	5/11	45
4-7gd	3/10	30
vector	1/10	10
none	1/9	11
Experiment 3		
21hw	2/11	18
22hw	3/12	25
23hw	2/12	17
24hw	2/12	17
25hw	0/10	0
21-25hw	7/12	58
vector	1/12	8
none	0/10	0